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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/918,508

DATE: 11/14/2001
TIME: 15:06:24

Input Set : A:\Q65478.app
Output Set: N:\CRF3\11142001\I918508.raw

3 <110> APPLICANT: KAKIMOTO, TATSUO
 4 HIGUCHI, MASAYUKI
 5 INOUE, TSUTOMU
 7 <120> TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
 8 TO CYTOKININ RECEPTOR
 10 <130> FILE REFERENCE: Q65478
 12 <140> CURRENT APPLICATION NUMBER: 09/918,508
 13 <141> CURRENT FILING DATE: 2001-08-01
 15 <150> PRIOR APPLICATION NUMBER: JP 2001-073812
 16 <151> PRIOR FILING DATE: 2001-03-15
 18 <160> NUMBER OF SEQ ID NOS: 22
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 3531
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Arabidopsis thaliana
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (1)..(3531)
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 34 1 5 10 15
 36 aag tcg tcg agc agt gac aag aaa tgg cta aag aag cct ctc ttc ttc 96
 37 Lys Ser Ser Ser Asp Lys Lys Trp Leu Lys Lys Pro Leu Phe Phe
 38 20 25 30
 40 ctg att ttg tgt ggc tct ttg gta att gtt ttg gtt atg ttc tta cg 144
 41 Leu Ile Leu Cys Gly Ser Leu Val Ile Val Leu Val Met Phe Leu Arg
 42 35 40 45
 44 tta ggt aga agt cag aag gag gag aca gat tct tgt aat gga gaa gag 192
 45 Leu Gly Arg Ser Gln Lys Glu Glu Thr Asp Ser Cys Asn Gly Glu Glu
 46 50 55 60
 48 aaa gtg ttg tat aga cat caa aat gtc aca aga agt gag att cat gat 240
 49 Lys Val Leu Tyr Arg His Gln Asn Val Thr Arg Ser Glu Ile His Asp
 50 65 70 75 80
 52 ttg gtc tct ttg ttc tct gat tca gat cag gta aca tcc ttt gaa tgt 288
 53 Leu Val Ser Leu Phe Ser Asp Ser Asp Gln Val Thr Ser Phe Glu Cys
 54 85 90 95
 56 cat aag gaa tca agc cct gga atg tgg aca aac tat ggt att aca tgt 336
 57 His Lys Glu Ser Ser Pro Gly Met Trp Thr Asn Tyr Gly Ile Thr Cys
 58 100 105 110
 60 tcc ctg agt gtg cgt tct gat aaa caa gag act aga ggg ctt ccc tgg 384
 61 Ser Leu Ser Val Arg Ser Asp Lys Gln Glu Thr Arg Gly Leu Pro Trp
 62 115 120 125
 64 aat ctt ggc tta gga cat tct atc tca tca aca tct tgt atg tgt ggt 432
 65 Asn Leu Gly Leu Gly His Ser Ile Ser Ser Thr Ser Cys Met Cys Gly
 66 130 135 140

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70	145 150 155 160	
72	cat gaa gaa ggg ctg gag cag ggt ttg tca tcg tat tta aga aat gca	528
73	His Glu Glu Gly Leu Glu Gln Gly Leu Ser Ser Tyr Leu Arg Asn Ala	
74	165 170 175	
76	tgg tgg tgt cta atc ctt ggt gtg tta gtg tgc cat aag att tat gta	576
77	Trp Trp Cys Leu Ile Leu Gly Val Leu Val Cys His Lys Ile Tyr Val	
78	180 185 190	
80	tct cat tct aaa gca cga ggt gag agg aaa gag aaa gta cat ctg caa	624
81	Ser His Ser Lys Ala Arg Gly Glu Arg Lys Glu Lys Val His Leu Gln	
82	195 200 205	
84	gag gct tta gct cca aag aag cag caa caa cgt gct cag act tct tct	672
85	Glu Ala Leu Ala Pro Lys Lys Gln Gln Arg Ala Gln Thr Ser Ser	
86	210 215 220	
88	aga ggg gct gga aga tgg agg aag aat atc ctt ctc ctt ggt att tta	720
89	Arg Gly Ala Gly Arg Trp Arg Lys Asn Ile Leu Leu Gly Ile Leu	
90	225 230 235 240	
92	gga gga gtt tcc ttc tct gtt tgg ttt tgg gac act aat gag gag	768
93	Gly Gly Val Ser Phe Ser Val Trp Trp Phe Trp Asp Thr Asn Glu Glu	
94	245 250 255	
96	atc ata atg aaa agg agg gag act ttg gca aac atg tgt gac gaa cga	816
97	Ile Ile Met Lys Arg Arg Glu Thr Leu Ala Asn Met Cys Asp Glu Arg	
98	260 265 270	
100	gca cgt gtt tta caa gat cag ttc aat gtt agc ttg aac cat gtt cat	864
101	Ala Arg Val Leu Gln Asp Gln Phe Asn Val Ser Leu Asn His Val His	
102	275 280 285	
104	gcc ttg tct att ctt gta tct aca ttt cat cat ggt aaa atc cca tct	912
105	Ala Leu Ser Ile Leu Val Ser Thr Phe His His Gly Lys Ile Pro Ser	
106	290 295 300	
108	gcc att gat cag aga aca ttt gaa gaa tat act gag aga aca aac ttt	960
109	Ala Ile Asp Gln Arg Thr Phe Glu Glu Tyr Thr Glu Arg Thr Asn Phe	
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112	gag agg cca ctt act agt ggt gta gcg tat gct ttg aaa gtc cca cac	1008
113	Glu Arg Pro Leu Thr Ser Gly Val Ala Tyr Ala Leu Lys Val Pro His	
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116	tca gaa aga gag aaa ttt gaa aag gag cat gga tgg gca ata aag aaa	1056
117	Ser Glu Arg Glu Lys Phe Glu Lys Glu His Gly Trp Ala Ile Lys Lys	
118	340 345 350	
120	atg gaa act gag gac cag aca gtt gta caa gat tgt gtt cct gaa aac	1104
121	Met Glu Thr Glu Asp Gln Thr Val Val Gln Asp Cys Val Pro Glu Asn	
122	355 360 365	
124	ttt gat ccc gca ccg att caa gac gaa tac gcg cca gtt ata ttt gct	1152
125	Phe Asp Pro Ala Pro Ile Gln Asp Glu Tyr Ala Pro Val Ile Phe Ala	
126	370 375 380	
128	caa gaa act gtt tcc cat att gta tcg gtc gac atg atg tct gga gaa	1200
129	Gln Glu Thr Val Ser His Ile Val Ser Val Asp Met Met Ser Gly Glu	
130	385 390 395 400	
132	gaa gac cgt gaa aac atc tta cgg gca agg gca tca gga aaa gga gtg	1248

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136	tta	aca	tct	cca	ttt	aag	ctt	aat	cat	ctt	ggt	gtt	gtg				1296
137	Leu	Thr	Ser	Pro	Phe	Lys	Leu	Leu	Lys	Ser	Asn	His	Leu	Gly	Val	Val	
138																	420
																	425
																	430
140	ttg	acc	ttt	gct	gtc	tat	gac	acg	agc	cta	ccg	cct	gat	gct	aca	gaa	1344
141	Leu	Thr	Phe	Ala	Val	Tyr	Asp	Thr	Ser	Leu	Pro	Pro	Asp	Ala	Thr	Glu	
142																	435
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																	445
144	gaa	cag	cgt	gtt	gaa	gca	act	att	ggg	tac	ctt	ggt	gca	tca	tat	gat	1392
145	Glu	Gln	Arg	Val	Glu	Ala	Thr	Ile	Gly	Tyr	Leu	Gly	Ala	Ser	Tyr	Asp	
146																	450
																	455
																	460
148	atg	cca	tcg	ctg	gtg	gag	aaa	ctt	ctt	cac	caa	ctt	gcc	agc	aaa	cag	1440
149	Met	Pro	Ser	Ieu	Val	Glu	Lys	Leu	Leu	His	Gln	Leu	Ala	Ser	Lys	Gln	
150																	465
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																	475
																	480
152	aca	att	gct	gtg	gat	gtt	tac	gac	aca	act	aac	act	tca	ggt	cta	ata	1488
153	Thr	Ile	Ala	Val	Asp	Val	Tyr	Asp	Thr	Thr	Asn	Thr	Ser	Gly	Leu	Ile	
154																	485
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																	495
156	aaa	atg	tat	ggc	tca	gaa	att	ggg	gat	ata	agt	gag	cag	cat	ata	agt	1536
157	Lys	Met	Tyr	Gly	Ser	Glu	Ile	Gly	Asp	Ile	Ser	Glu	Gln	His	Ile	Ser	
158																	500
																	505
																	510
160	agc	ctt	gat	ttt	ggt	gat	cca	tca	agg	aac	cat	gag	atg	cat	tgc	agg	1584
161	Ser	Leu	Asp	Phe	Gly	Asp	Pro	Ser	Arg	Asn	His	Glu	Met	His	Cys	Arg	.
162																	515
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164	ttt	aag	cat	aaa	ctt	ccc	att	ccc	tgg	aca	gcg	ata	aca	ccg	tcg	atc	1632
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166																	530
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169	Leu	Val	Leu	Val	Ile	Thr	Phe	Leu	Val	Gly	Tyr	Ile	Leu	Tyr	Glu	Ala	
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																	550
																	555
																	560
172	atc	aac	cga	att	gcg	aca	gta	ggg	gag	gat	tgt	cag	aag	atg	agg	gaa	1728
173	Ile	Asn	Arg	Ile	Ala	Thr	Val	Glu	Glu	Asp	Cys	Gln	Lys	Met	Arg	Glu	
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																	575
176	ctc	aaa	gct	cgt	gct	gag	gcc	gct	gac	att	gca	aag	tca	cag	ttc	cta	1776
177	Leu	Lys	Ala	Arg	Ala	Glu	Ala	Ala	Asp	Ile	Ala	Lys	Ser	Gln	Phe	Leu	
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																	590
180	gca	act	gtt	tct	cat	gag	ata	cg	act	ccg	atg	aat	gga	gtt	tta	gga	1824
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189	Tyr	Ala	Gln	Thr	Ala	His	Gly	Ser	Gly	Lys	Asp	Leu	Thr	Ser	Leu	Ile	
190																	625
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192	aat	gag	gtt	ctt	gat	cag	gca	aag	att	gaa	tcc	gga	agg	ctc	gag	ctt	1968
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204	gtt tct agt caa gtt cct gat gtt gta gtc ggt gat ccg agt cgg ttc			2112
205	Val Ser Ser Gln Val Pro Asp Val Val Val Gly Asp Pro Ser Arg Phe			
206	690	695	700	
208	cgg cag atc att aca aac ctg gtt gga aac tca atc aaa ttc aca cag			2160
209	Arg Gln Ile Ile Thr Asn Leu Val Gly Asn Ser Ile Lys Phe Thr Gln			
210	705	710	715	720
212	gaa agg gga cac ata ttt atc tca gtg cac ctt gca gat gag gta aag			2208
213	Glu Arg Gly His Ile Phe Ile Ser Val His Leu Ala Asp Glu Val Lys			
214	725	730	735	
216	gag cct ctt act att gaa gac gca gtg cta aaa cag cga cta gct tta			2256
217	Glu Pro Leu Thr Ile Glu Asp Ala Val Leu Lys Gln Arg Leu Ala Leu			
218	740	745	750	
220	gga tgc agc gag tcc ggt gag aca gtt agc ggg ttt cct gcg gta aat			2304
221	Gly Cys Ser Glu Ser Gly Glu Thr Val Ser Gly Phe Pro Ala Val Asn			
222	755	760	765	
224	gca tgg gga agc tgg aag aat ttc aag aca tgt tac agt act gag agt			2352
225	Ala Trp Gly Ser Trp Lys Asn Phe Lys Thr Cys Tyr Ser Thr Glu Ser			
226	770	775	780	
228	cag aat tct gat caa atc aaa ttg cta gtt aca gtg gag gac act gga			2400
229	Gln Asn Ser Asp Gln Ile Lys Leu Leu Val Thr Val Glu Asp Thr Gly			
230	785	790	795	800
232	gtt ggc ata cct gtg gat gca caa ggc cga atc ttc aca cct ttt atg			2448
233	Val Gly Ile Pro Val Asp Ala Gln Gly Arg Ile Phe Thr Pro Phe Met			
234	805	810	815	
236	caa gcc gac agt tcc aca tcg cgg act tat ggt gga act ggc ata ggt			2496
237	Gln Ala Asp Ser Ser Thr Ser Arg Thr Tyr Gly Gly Thr Gly Ile Gly			
238	820	825	830	
240	ttg agt ata agc aaa cgt ttg gtt gaa ctc atg caa gga gag atg ggg			2544
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244	ttt gtg agt gag ccc ggg ata ggc agt act ttt tca ttt act gga gtt			2592
245	Phe Val Ser Glu Pro Gly Ile Gly Ser Thr Phe Ser Phe Thr Gly Val			
246	850	855	860	
248	tcc ggg aaa gca gaa aca aat acg tcg att act aag ctg gaa cga ttc			2640
249	Phe Gly Lys Ala Glu Thr Asn Thr Ser Ile Thr Lys Leu Glu Arg Phe			
250	865	870	875	880
252	gat cta gct att cag gag ttt aca gga ttg aga gca tta gtt att gat			2688
253	Asp Leu Ala Ile Gln Glu Phe Thr Gly Leu Arg Ala Leu Val Ile Asp			
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256	aac aga aac att aga gca gag gtc acc agg tac gaa ctt cgg aga ctg			2736
257	Asn Arg Asn Ile Arg Ala Glu Val Thr Arg Tyr Glu Leu Arg Arg Leu			
258	900	905	910	
260	gga ata tct gca gac att gtt tca agt ctg aga atg gca tgc act tgt			2784
261	Gly Ile Ser Ala Asp Ile Val Ser Ser Leu Arg Met Ala Cys Thr Cys			
262	915	920	925	

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266	930 935 940	
268	gcc tgg aac aag gaa gaa ttt tca gta ctt gac gag ttg ttt acc cga	2880
269	Ala Trp Asn Lys Glu Glu Phe Ser Val Leu Asp Glu Leu Phe Thr Arg	
270	945 950 955 960	
272	agc aaa gta acc ttt aca aga gtc cca aag att ttt ctt ttg gca act	2928
273	Ser Lys Val Thr Phe Thr Arg Val Pro Lys Ile Phe Leu Leu Ala Thr	
274	965 970 975	
276	tct gca act ctt act gag cgc agt gag atg aag tct act ggt ctc atc	2976
277	Ser Ala Thr Leu Thr Glu Arg Ser Glu Met Lys Ser Thr Gly Leu Ile	
278	980 985 990	
280	gat gag gtg gtg ata aag cct ctt cg ^g atg agt gtc tta ata tgt tgc	3024
281	Asp Glu Val Val Ile Lys Pro Leu Arg Met Ser Val Leu Ile Cys Cys	
282	995 1000 1005	
284	ttg caa gaa acc ctt gtc aat ggc aag aag agg caa ccg aac aga cag	3072
285	Leu Gln Glu Thr Leu Val Asn Gly Lys Lys Arg Gln Pro Asn Arg Gln	
286	1010 1015 1020	
288	cga aga aat ctt gga cac ttg cta aga gaa aaa cag att ctg gtt gtg	3120
289	Arg Arg Asn Leu Gly His Leu Leu Arg Glu Lys Gln Ile Leu Val Val	
290	1025 1030 1035 1040	
292	gat gat aat ctt gtg aac aga cga gtt gca gaa ggt gca ctt aag aaa	3168
293	Asp Asp Asn Leu Val Asn Arg Arg Val Ala Glu Gly Ala Leu Lys Lys	
294	1045 1050 1055	
296	tat gga gct att gtt aca tgc gtt gag agt ggc aaa gct gca ttg gca	3216
297	Tyr Gly Ala Ile Val Thr Cys Val Glu Ser Gly Lys Ala Ala Leu Ala	
298	1060 1065 1070	
300	atg ctt aag ccg cct cat aac ttc gat gct tgc ttc atg gat ctc cag	3264
301	Met Leu Lys Pro Pro His Asn Phe Asp Ala Cys Phe Met Asp Leu Gln	
302	1075 1080 1085	
304	atg cct gaa atg gat gga ttt gaa gcg aca agg aga gtc cgt gag ctg	3312
305	Met Pro Glu Met Asp Gly Phe Glu Ala Thr Arg Arg Val Arg Glu Leu	
306	1090 1095 1100	
308	gag agg gaa atc aat aag aaa ata gct tct gga gaa gtt tca gct gaa	3360
309	Glu Arg Glu Ile Asn Lys Lys Ile Ala Ser Gly Glu Val Ser Ala Glu	
310	1105 1110 1115 1120	
312	atg ttc tgt aaa ttt agt agt tgg cac gtc ccg ata tta gca atg aca	3408
313	Met Phe Cys Lys Phe Ser Ser Trp His Val Pro Ile Leu Ala Met Thr	
314	1125 1130 1135	
316	gca gat gtt att cag gct act cat gaa gaa tgc atg aaa tgt gga atg	3456
317	Ala Asp Val Ile Gln Ala Thr His Glu Glu Cys Met Lys Cys Gly Met	
318	1140 1145 1150	
320	gat ggt tat gta tca aaa ccg ttt gaa gag gaa gtg ctc tac aca gcg	3504
321	Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Val Leu Tyr Thr Ala	
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326	1170 1175	
329	<210> SEQ ID NO: 2	

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